

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/714, 353 B
Source: IFW16
Date Processed by STIC: 02/13/2007

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IFW16

RAW SEQUENCE LISTING

DATE: 02/13/2007

PATENT APPLICATION: US/10/714,353B

TIME: 10:05:43

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02132007\J714353B.raw

3 <110> APPLICANT: SCHUURMAN, JANINE
 4 HAVENITH, KARIN
 5 PARREN, PAUL
 6 VAN DE WINKEL, JAN
 7 WILLIAMS, DENISE LEAH
 8 PETERSEN, JORGEN
 9 BAADSGAARD, OLE
 11 <120> TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD25
 13 <130> FILE REFERENCE: GMI-059
 15 <140> CURRENT APPLICATION NUMBER: 10/714,353B
 16 <141> CURRENT FILING DATE: 2003-11-14
 18 <150> PRIOR APPLICATION NUMBER: 60/426,690
 19 <151> PRIOR FILING DATE: 2002-11-15
 21 <160> NUMBER OF SEQ ID NOS: 74
 23 <170> SOFTWARE: PatentIn Ver. 3.3
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 381
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(381)
 34 <400> SEQUENCE: 1

35 cag gtt cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg tcc 48
 36 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 37 1 5 10 15
 39 tcg gtg aaa gtc tcc tgc aag gct tct gga ggc acc ttc agc cgt tat 96
 40 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr
 41 20 25 30
 43 cct atc aac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
 44 Pro Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 45 35 40 45
 47 gga agg atc atc cct atc ctt ggt ata gca gac tac gca cag agg ttc 192
 48 Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asp Tyr Ala Gln Arg Phe
 49 50 55 60
 51 cag ggc aga gtc acg att acc gcg gac aaa tcc acg aac aca gcc tac 240
 52 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr
 53 65 70 75 80
 55 atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tat tgt 288
 56 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 57 85 90 95
 59 gcg agg agg gac tgg gga gac tac tgg ggc cag gga acc ctg gtc acc 336
 60 Ala Arg Arg Asp Trp Gly Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr

CPS-6)

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61          100          105          110
63 gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca      381
64 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
65          115          120          125
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 127
70 <212> TYPE: PRT
71 <213> ORGANISM: Homo sapiens
73 <400> SEQUENCE: 2
74 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
75 1          5          10          15
77 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr
78          20          25          30
80 Pro Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
81          35          40          45
83 Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asp Tyr Ala Gln Arg Phe
84          50          55          60
86 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr
87 65          70          75          80
89 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
90          85          90          95
92 Ala Arg Arg Asp Trp Gly Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
93          100          105          110
95 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
96          115          120          125
100 <210> SEQ ID NO: 3
101 <211> LENGTH: 420
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
105 <220> FEATURE:
106 <221> NAME/KEY: CDS
107 <222> LOCATION: (1)..(420)
109 <400> SEQUENCE: 3
110 atg gaa gcc cca gca cag ctt ctc ttc ctc ctg cta ctc tgg ctc cca      48
111 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
112 1          5          10          15
114 gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg tct      96
115 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
116          20          25          30
118 ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt      144
119 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
120          35          40          45
122 gtt agc agc agc ttc tta gcc tgg tac cag cag aaa cct ggc cag gct      192
123 Val Ser Ser Ser Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
124          50          55          60
126 ccc agg ctc ctc atc tat ggt gca tcc agc agg gcc act ggc atc cca      240
127 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
128 65          70          75          80
130 gac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc      288

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131 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
132      85      90      95
134 agc aga ctg gag cct gaa gat ttt gca gtg tat tac tgt cag cag tat 336
135 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
136      100      105      110
138 agt agc tca ccg ctc act ttc ggc gga ggg acc aag gtg gag atc aaa 384
139 Ser Ser Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
140      115      120      125
142 cga act gtg gct gca cca tct gtc ttc atc ttc ccg 420
143 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
144      130      135      140
147 <210> SEQ ID NO: 4
148 <211> LENGTH: 140
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 4
153 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
154 1 5 10 15
156 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
157 20 25 30
159 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
160 35 40 45
162 Val Ser Ser Ser Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
163 50 55 60
165 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
166 65 70 75 80
168 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
169 85 90 95
171 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
172 100 105 110
174 Ser Ser Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
175 115 120 125
177 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
178 130 135 140
182 <210> SEQ ID NO: 5
183 <211> LENGTH: 381
184 <212> TYPE: DNA
185 <213> ORGANISM: Homo sapiens
187 <220> FEATURE:
188 <221> NAME/KEY: CDS
189 <222> LOCATION: (1)..(381)
191 <400> SEQUENCE: 5
192 cag gtt cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg tcc 48
193 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
194 1 5 10 15
196 tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc aga tat 96
197 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr
198 20 25 30
200 gct atc aac tgg gtg cga cag gcc cct gga caa gga ctt gag tgg atg 144

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201 Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
202          35          40          45
204 gga agg atc atc cct atc ctt gat ata gca gac tac gca cag aag ttc 192
205 Gly Arg Ile Ile Pro Ile Leu Asp Ile Ala Asp Tyr Ala Gln Lys Phe
206          50          55          60
208 cag gac aga gtc acg att acc gcg gac aag tcc acg aac aca gcc tac 240
209 Gln Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr
210 65          70          75          80
212 atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt 288
213 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
214          85          90          95
216 gcg aga aag gac tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc 336
217 Ala Arg Lys Asp Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
218          100          105          110
220 gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca 381
221 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
222          115          120          125
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 127
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
230 <400> SEQUENCE: 6
231 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
232 1          5          10          15
234 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr
235          20          25          30
237 Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
238          35          40          45
240 Gly Arg Ile Ile Pro Ile Leu Asp Ile Ala Asp Tyr Ala Gln Lys Phe
241          50          55          60
243 Gln Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr
244 65          70          75          80
246 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
247          85          90          95
249 Ala Arg Lys Asp Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
250          100          105          110
252 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
253          115          120          125
257 <210> SEQ ID NO: 7
258 <211> LENGTH: 420
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
262 <220> FEATURE:
263 <221> NAME/KEY: CDS
264 <222> LOCATION: (1)..(420)
266 <400> SEQUENCE: 7
267 atg gaa gcc cca gca cag ctt ctc ttc ctc ctg cta ctc tgg ctc cca 48
268 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
269 1          5          10          15

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271 gat atc acc gga gaa aat gtg ttg acg cag tct cca ggc acc ctg tct 96
272 Asp Ile Thr Gly Glu Asn Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
273          20          25          30
275 ctg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt 144
276 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
277          35          40          45
279 ggt agc agc agc tac tta gcc tgg tac cag cag aaa cct ggc cag gct 192
280 Gly Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
281          50          55          60
283 ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc act ggc atc cca 240
284 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
285 65          70          75          80
287 gac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc 288
288 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
289          85          90          95
291 agc aga ctg gag cct gaa gat ttt gca gtg tat tac tgt cag cag tat 336
292 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
293          100          105          110
295 ggt agt tca ccg atc acc ttc ggc caa ggg aca cga ctg gag att aaa 384
296 Gly Ser Ser Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
297          115          120          125
299 cga act gtg gct gca cca tct gtc ttc atc ttc ccc 420
300 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
301          130          135          140
304 <210> SEQ ID NO: 8
305 <211> LENGTH: 140
306 <212> TYPE: PRT
307 <213> ORGANISM: Homo sapiens
309 <400> SEQUENCE: 8
310 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
311 1          5          10          15
313 Asp Ile Thr Gly Glu Asn Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
314          20          25          30
316 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
317          35          40          45
319 Gly Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
320          50          55          60
322 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
323 65          70          75          80
325 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
326          85          90          95
328 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
329          100          105          110
331 Gly Ser Ser Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
332          115          120          125
334 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
335          130          135          140
339 <210> SEQ ID NO: 9
340 <211> LENGTH: 381

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/714,353B

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Input Set : A:\Sequence Listing.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:62; Xaa Pos. 3/
Seq#:63; Xaa Pos. 8,9,10,14,17
Seq#:64; Xaa Pos. 8,9,10,14,17
Seq#:65; Xaa Pos. 8,9,10,14,17
Seq#:66; Xaa Pos. 6,9
Seq#:67; Xaa Pos. 6,9
Seq#:68; Xaa Pos. 6,9
Seq#:69; Xaa Pos. 4,8,9
Seq#:70; Xaa Pos. 4,8
Seq#:73; Xaa Pos. 1,3,5
Seq#:74; Xaa Pos. 1,3,5

VERIFICATION SUMMARY

DATE: 02/13/2007

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Input Set : A:\Sequence Listing.txt

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L:1106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62 after pos.:0
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:0
M:341 Repeated in SeqNo=63
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:0
M:341 Repeated in SeqNo=64
L:1227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:0
M:341 Repeated in SeqNo=65
L:1252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0
L:1272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:0
L:1292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:0
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0
L:1337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0
L:1421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73 after pos.:0
L:1448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0